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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 100243

TO: Vanessa L Ford
Location: cm-1/8A16/8E12
Art Unit: 1645

Aug 4, 2003

Case Serial Number: 10/017168

From: P. Sheppard
Location: CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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From: Chan, Christina
Sent: Thursday, July 31, 2003 3:35 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: In re: 10/017168 sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Ford, Vanessa
Sent: Thursday, July 31, 2003 2:49 PM
To: Chan, Christina
Subject: In re: 10/017168 sequence search

Please search SEQ ID NO:15. Please include interference searches. Please rush!

Vanessa L. Ford
Biotechnology Patent Examiner
Office: CM1 8A16
Mailbox: CM1 8E12
Phone: 703.308.4735

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JUL 31 2003
STIC

Point of Contact
P. Sheppard
telephone number: (703) 308-4499

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 8/4/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2003, 18:26:45 ; Search time 95 seconds
(without alignments)
54.327 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101

Sequence: 1 EVEDPKVPEPASEGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mmc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_prodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	348	2 Q9ALV7	Q9ALV7 treponema p
2	101	100.0	393	2 Q9JCA3	Q9JCA3 treponema p
3	101	100.0	428	2 Q9ALV6	Q9ALV6 treponema p
4	101	100.0	432	2 O51953	O51953 treponema p
5	101	100.0	548	2 Q9JCA4	Q9JCA4 treponema p
6	97	96.0	256	16 Q83448	Q83448 treponema p
7	82	81.2	227	16 Q83449	Q83449 treponema p
8	50	49.5	187	10 Q9J1I8	Q9J1I8 arabisidopsis
9	50	49.5	193	10 Q9J1I5	Q9J1I5 arabisidopsis
10	49	48.5	256	4 Q8WV22	Q8WV22 homo sapien
11	48	47.5	547	16 P95090	P95090 mycobacteri
12	48	47.5	2192	5 Q81BW7	Q81BW7 plasmodium
13	47.5	47.0	792	16 Q8CPY0	Q8CPY0 staphylococ
14	47	46.5	266	11 Q9D720	Q9D720 mus musculu
15	47	46.5	280	11 Q8K2B4	Q8K2B4 mus musculu
16	47	46.5	280	11 Q9CY20	Q9CY20 mus musculu

17	47	46.5	308	12 Q98494	Q98494 paramacium
18	47	46.5	650	4 Q81Y36	Q81Y36 homo sapien
19	47	46.5	685	5 Q9J381	Q9J381 caenorhabdi
20	47	46.5	1151	5 Q9XUR2	Q9XUR2 caenorhabdi
21	47	46.5	1159	12 Q9IMX8	Q9IMX8 cercopithec
22	47	46.5	1386	4 Q8C0A3	Q8C0A3 homo sapien
23	46.5	46.0	946	10 Q9LP09	Q9LP09 arabisidopsis
24	46	45.5	174	10 Q8W325	Q8W325 oryza sativ
25	46	45.5	348	4 Q8N446	Q8N446 homo sapien
26	46	45.5	383	2 Q93CV7	Q93CV7 lactobacilli
27	46	45.5	434	10 Q93X74	Q93X74 brassica ra
28	46	45.5	779	4 Q9H348	Q9H348 homo sapien
29	46	45.5	849	11 Q8CG01	Q8CG01 mus musculu
30	46	45.5	853	11 Q8CJ33	Q8CJ33 mus musculu
31	46	45.5	853	11 Q8BK66	Q8BK66 mus musculu
32	45	44.6	99	5 Q23793	Q23793 chironomus
33	45	44.6	99	5 Q23794	Q23794 chironomus
34	45	44.6	178	16 Q92UB5	Q92UB5 thizobium m
35	45	44.6	193	16 Q8PQY1	Q8PQY1 xanthomonas
36	45	44.6	264	16 Q31775	Q31775 bacillus su
37	45	44.6	286	2 Q9ANA3	Q9ANA3 bradyrhizob
38	45	44.6	286	10 Q8L7T9	Q8L7T9 arabisidopsis
39	45	44.6	294	10 Q9PFT7	Q9PFT7 arabisidopsis
40	45	44.6	379	6 Q9GLI3	Q9GLI3 macropus ru
41	45	44.6	474	17 Q96YS8	Q96YS8 sulfolobus
42	45	44.6	483	12 Q9JGT4	Q9JGT4 northern ce
43	45	44.6	798	5 Q45181	Q45181 caenorhabdi
44	45	44.6	873	5 Q20072	Q20072 caenorhabdi
45	44.5	44.1	243	17 Q8TY79	Q8TY79 methanopyru

ALIGNMENTS

RESULT 1

Q9ALV7 PRELIMINARY; PRT; 348 AA.

AC Q9ALV7;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Acidic repeat protein.

GN ARP.

OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI_TaxID=168;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CD2;

RA Liu H., Steiner B.M., Rodas B.;

RT "Molecular characterization of the acidic repeat protein (arp) of Treponema pallidum."

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CD2;

RA Liu H., Steiner B.;

RT "Acidic repeat protein (arp) gene sequence of Treponema pallidum subsp. pertenue (CDC 2 strain)."

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF342806; AAK01460.2; -

SQ SEQUENCE 348 AA; 37936 MW; EAA446BD82344592 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 2.2e-07;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDPKVPEPASEGGER 20

|||||

DB 128 EVEDPKVPEPASEGGER 147

RESULT 2

Q93CA3 PRELIMINARY; PRT; 393 AA.
 ID Q93CA3
 AC Q93CA3;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Acidic repeat protein.
 GN ARP.
 OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=168;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDCl;
 RA Liu H., Steiner B.M., Rodas B.;
 RT "Molecular characterization of the acidic repeat protein gene (arp) of
 Treponema pallidum.";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF411126; AAL07373.1; -
 SQ SEQUENCE 393 AA; 42852 MW; C2D9198AA1BB82B5 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEASEREGGER 20
 DB 133 EVEDVPKVVPEASEREGGER 152

RESULT 3
 Q9ALV6 PRELIMINARY; PRT; 428 AA.

ID Q9ALV6
 AC Q9ALV6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Acidic repeat protein.
 GN ARP.

OS Treponema pallidum subsp. endemicum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=53436;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bosnia;
 RA Liu H., Steiner B.M., Rodas B.;

RT "Molecular characterization of the acidic repeat protein (arp) of
 Treponema pallidum.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF342807; AAK01461.2; -
 SQ SEQUENCE 428 AA; 46710 MW; B14ED8A074D4333 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 428;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEASEREGGER 20
 DB 128 EVEDVPKVVPEASEREGGER 147

RESULT 4
 ID Q91953 PRELIMINARY; PRT; 432 AA.
 AC Q91953;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Acidic repeat protein.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RA Steiner B.M., Liu H., Rodas B.;
 RT "Characterization of an Acidic Repeat Protein from Treponema
 pallidum.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF015824; AAB94541.1; -
 SQ SEQUENCE 432 AA; 46364 MW; 8FE1B4C55CE46A23 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 432;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEASEREGGER 20
 DB 168 EVEDVPKVVPEASEREGGER 187

RESULT 5
 Q93CA4 PRELIMINARY; PRT; 548 AA.

ID Q93CA4
 AC Q93CA4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Acidic repeat protein.
 GN ARP.

OS Treponema pallidum subsp. pallidum (syphilis treponeme).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=161;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Nichols;
 RA Liu H., Steiner B.M., Rodas B.;
 RT "Molecular characterization of the acidic repeat protein gene (arp) of
 Treponema pallidum.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF411124; AAL07372.1; -
 SQ SEQUENCE 548 AA; 59405 MW; 1F6B5BB04D41D13 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEASEREGGER 20
 DB 168 EVEDVPKVVPEASEREGGER 187

RESULT 6
 ID Q83448 PRELIMINARY; PRT; 256 AA.

ID Q83448
 AC Q83448;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein TP0433.
 GN TP0433.

OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.;


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RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uteback T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT Spirochete.";
RL Science 281:375-388(1998).
DR EMBL; AE001220; AAC65421.1; -.
DR TIGR; TP0433; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;

Query Match 96.0%; Score 97; DB 16; Length 256;
Best Local Similarity 95.0%; Pred. No. 6.6e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVEDVPKVVPEPASPAREGGER 20
Db 184 EVEDAPKVVPEPASPAREGGER 203

RESULT 7
083449 PRELIMINARY; PRT; 227 AA.
AC 083449;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein TP0434.
GN TP0434.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
CX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uteback T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT Spirochete.";
RL Science 281:375-388(1998).
DR EMBL; AE001220; AAC65422.1; -.
DR TIGR; TP0434; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 227 AA; 25035 MW; 3FA02711A6B8A5FB CRC64;

Query Match 81.2%; Score 82; DB 16; Length 227;
Best Local Similarity 85.0%; Pred. No. 0.00012;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVEDVPKVVPEPASPAREGGER 20
Db 47 EVEDVPKVVPEPASPAREGGER 66

RESULT 8
095178 PRELIMINARY; PRT; 187 AA.
AC 095178;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Expressed protein (RD2 protein).
GN AT2621620.
OS Arabidopsis thaliana (Mouse-ear cress).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Bannstead M.E., Mason T.M., Bowman C.L., Roming C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (F8B-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007119; AAD23643.2; -.
DR EMBL; AY087097; AAM64657.1; -.
DR InterPro; IPR006016; Usp_dom.
DR Pfam; PF00582; Usp; 1.
SQ SEQUENCE 187 AA; 20587 MW; BC8146F9BC802B76 CRC64;

Query Match 49.5%; Score 50; DB 10; Length 187;
Best Local Similarity 62.5%; Pred. No. 8.9;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 VPKVPEPASPAREGGER 20
Db 21 IPVVPPEPASPAREGGER 36

RESULT 9
094115 PRELIMINARY; PRT; 193 AA.
AC 094115;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE RD2 protein.
GN RD2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Shinzaki K., Yamaguchi-Shinozaki K., Takahashi S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Yamaguchi-Shinozaki K., Koizumi M., Urao S., Shinzaki K.;
RT "Molecular cloning and characterization of 9 cDNAs for genes that are
RT responsive to desiccation in Arabidopsis thaliana: sequence analysis
RT of one cDNA clone that encodes a putative transmembrane channel
RT protein.";
RL Plant Cell Physiol. 33:217-224(1992).
DR EMBL; AB039925; BAB63912.1; -.
DR InterPro; IPR006016; Usp_dom.
DR Pfam; PF00582; Usp; 1.
SQ SEQUENCE 193 AA; 21253 MW; EAA5F1D0BFED679 CRC64;

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Query Match 49.5%; Score 50; DB 10; Length 193;
 Best Local Similarity 62.5%; Pred. No. 9.2;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 VKVPEPASERGGC 20
 DB 21 IPVPEPELERSGGR 36

RESULT 10

Q8WV22 PRELIMINARY; PRT; 256 AA.

AC Q8WV22
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 OS Similar to RIKEN CDNA 2510027N19 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancrreas;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC018938; AAH18938.1; -
 DR InterPro: IPR000345; Cyt_c_heme_bind.
 DR InterPro: IPR002219; DAG_Pe_bind.
 DR InterPro: IPR001841; ZnF_Ting.
 DR PROSITE: PS00190; CYTOCHROME_C_1.
 DR PROSITE: PS50081; DAG_Pe_BIND_DOM_2; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 256 AA; 29724 MW; 3433001005D7EDDF CRC64;

Query Match 48.5%; Score 49; DB 4; Length 256;
 Best Local Similarity 53.3%; Pred. No. 18;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 DVKVPASERREG 18
 DB 228 EIKVPDFEKRBSG 242

RESULT 11

P95090 PRELIMINARY; PRT; 547 AA.

AC P95090
 DT 01-MAY-1997 (TRENBLREL. 03, Created)
 DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Hypothetical 58.3 kDa protein (Phosphoglucosyltransferase).
 GN PGMA OR RV3068C OR MTCY22D7.13 OR MT3153.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 RN NCBI_TaxID=1773;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla F.,
 RA Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagers K., Krogan A., McLean J., Moule S., Murphy J.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544 (1998).
 [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z83866; CAB06255.1; -
 DR EMBL: AE007132; AAK47488.1; -
 DR TIGR: MT3153; -
 DR Tuberculosis; RV3068C; -
 DR InterPro: IPR005841; PG_PMM_mutase.
 DR InterPro: IPR005852; Pglucmutase A.
 DR InterPro: IPR005844; PG_PMM_ABAI.
 DR InterPro: IPR005845; PG_PMM_ABAII.
 DR InterPro: IPR005846; PG_PMM_ABAIII.
 DR InterPro: IPR005843; PG_PMM_C.
 DR Pfam: PF00408; PGM_PMM_1.
 DR Pfam: PF02878; PGM_PMM_1; 1.
 DR Pfam: PF02879; PGM_PMM_1; 1.
 DR Pfam: PF02880; PGM_PMM_1; 1.
 DR TIGRfam: TIGR01132; Pgm; 1.
 DR PROSITE: PS00710; PGM_PMM; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 547 AA; 58265 MW; 1825BDD8E9A95951 CRC64;

Query Match 47.5%; Score 48; DB 16; Length 547;
 Best Local Similarity 52.6%; Pred. No. 56;
 Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 VEDVPKVPASERGGC 20
 DB 210 VDDLPNVVDIAIRAGVR 228

RESULT 12

Q81BW7 PRELIMINARY; PRT; 2192 AA.

AC Q81BW7
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Erythrocyte membrane protein 1 (PEM1).
 GN MAL7P1.56.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN NCBI_TaxID=36329;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
 RA Quail M., Barrett B.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL844506; CAD50877.1; -
 SQ SEQUENCE 2192 AA; 248940 MW; 4EAD66FF62A81329 CRC64;

Query Match 47.5%; Score 48; DB 5; Length 2192;
 Best Local Similarity 56.2%; Pred. No. 2.5e+02;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVEDVPKVPASER 16
 DB 877 EKEKAPKVPAPVKE 892

RESULT 13

Q8CPY0 PRELIMINARY; PRT; 792 AA.

AC Q8CPY0
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)

```
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE Ribonuclease R.
GN SE0565.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Xu Y., Qin Z.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016745; AA004162.1; -.
KW Complete proteome.
SQ SEQUENCE 792 AA; 91110 MW; E83F9C4C98AB7D7F CRC64;

Query Match          47.0%; Score 47.5; DB 16; Length 792;
Best Local Similarity 64.7%; Pred. No. 1e+02;
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 EVDVPKVPEPASEREG 17
DB 235 EAEVDPVIEP-SEIEG 250

RESULT 14
Q9D720 PRELIMINARY; PRT; 266 AA.
ID Q9D720.
AC Q9D720.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 2510027N19R1K protein.
GN 2510027N19R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanao I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Farsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brenner M., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009715; BAB26459.1; -.
DR MGI; MGI:1914961; 2510027N19R1K.
DR InterPro; IPR000345; CyC_heme_bind.
DR InterPro; IPR002219; DAG_Pe-bind.
DR PROSITE; PS00190; CYTOCHROME_C_1.
DR PROSITE; PS50081; DAG_Pe_BIND_DOM_2; 1.
SQ SEQUENCE 266 AA; 30708 MW; F5728C530532E03A CRC64;

Query Match          46.5%; Score 47; DB 11; Length 266;
Best Local Similarity 53.3%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 4 DVPKVPPEPASEREG 18
DB 238 DIPVYNPEKEREAG 252

RESULT 15
Q8K2B4 PRELIMINARY; PRT; 280 AA.
ID Q8K2B4.
AC Q8K2B4.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RIKEN cDNA 2510027N19 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031848; AAH31848.1; -.
DR InterPro; IPR000345; CyC_heme_bind.
DR InterPro; IPR002219; DAG_Pe-bind.
DR PROSITE; PS00190; CYTOCHROME_C_1.
DR PROSITE; PS50081; DAG_Pe_BIND_DOM_2; 1.
SQ SEQUENCE 280 AA; 32038 MW; CC5BCCC949EA269F CRC64;

Query Match          46.5%; Score 47; DB 11; Length 280;
Best Local Similarity 53.3%; Pred. No. 40;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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Search completed: August 1, 2003, 18:36:13
Job time : 98 secs

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DT 01-AUG-1991 (Rel. 19, Last sequence update)
DR 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrase (Recombinase).
GN INT.
OS Saccharopolyspora erythraea (Streptomyces erythraeus).
OG Plasmid pSE211.
OC Bacteria; Actinobacteria; Actinomycetaceae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiales; Saccharopolyspora.
RX NCBI_TaxID=1836;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=90202705; PubMed=2180909;
RA Brown D.P., Idler K.B., Katz L.;
RT "Characterization of the genetic elements required for site-specific
RT integration of plasmid pSE211 in Saccharopolyspora erythraea.";
RL J. Bacteriol. 172:1877-1888(1990).
CC -1- FUNCTION: Is a recombinase (or integrase), catalyzing the cutting
CC and rejoining of the recombinating DNA molecules.
CC -1- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
CC -----
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CC -----
DR EMBL, M51518; AAA89345.1; -.
DR F01R, C35147; C35147.
DR InterPro; IPR002104; Phage integrase.
DR Pfam; PF00589; Phage integrase; 1.
KW DNA recombination; DNA integration; Plasmid.
FT ACT_SITE 414 414 TRANSIENT COVALENT LINKAGE TO DNA DURING
FT STRAND CLEAVAGE AND REJOINING (BY
FT SIMILARITY).
SQ SEQUENCE 437 AA; 50323 MW; 29EBD7108CC5AFBD CRC64;
QY 1 EYEDVPKVPASEREGE 20
DB 185 EYEDMQLVTKALERANGVR 204

Query Match 45.5%; Score 46; DB 1; Length 437;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

RESULT 3
VP41_HUMAN STANDARD; PRT; 854 AA.
AC P49754; Q99851; Q99852;
ID 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vacuolar assembly protein VPS41 homolog (S53).
GN VPS41.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Heart;
RC TISSUE=Heart;
RX MEDLINE=97303186; PubMed=9159129;
RA Radisky D.C., Snyder W.B., Emr S.D., Kaplan J.;
RT "Characterization of VPS41, a gene required for vacuolar trafficking
RT and high-affinity iron transport in yeast.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:5662-5666(1997).
[2]
RP SEQUENCE OF 615-744 FROM N.A.
RC TISSUE=Brain;
RC MEDLINE=95319502; PubMed=7596406;
RA Sherrington R., Rogaeva E.I., Liang Y., Rogaeva E.A., Levesque G.,

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RA Ikeda M., Chi H., Iin C., Li G., Holman K., Tsuda T., Mar L.,
RA Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rahero I.,
RA Pinassi L., Nee L., Chumakov I., Pollen D., Brookes A.,
RA Saneau P., Polinsky R.J., Maeco W., da Silva H.A.R., Haines J.L.,
RA Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
RA Rommens J.M., St George-Hyslop P.H.;
RT "Cloning of a gene bearing missense mutations in early-onset familial
RT Alzheimer's disease.";
RL Nature 375:754-760(1995).
CC -1- FUNCTION: REQUIRED FOR VACUOLAR ASSEMBLY AND VACUOLAR TRAFFIC.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC Name=Short;
CC IsoId=P49754-1; Sequence=Displayed;
CC IsoId=P49754-2; Sequence=VSP_006751, VSP_006752;
CC -1- SIMILARITY: BELONGS TO THE VPS41 FAMILY.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
DR EMBL, U87309; AAA7563.1; -.
DR EMBL, U87281; AAA7758.1; -.
DR EMBL, L40398; AAC42004.1; -.
DR Genew; HGNC:12713; VPS41.
DR MIM; 605485; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005478; F:intracellular transporter activity; TAS.
DR GO; GO:0007034; P:vacuolar transport; TAS.
DR InterPro; IPR000547; Clathrin_repeat.
DR InterPro; IPR001841; Znf ring.
DR Pfam; PF00637; Clathrin; 1.
DR SMART; SM00299; CLH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Zinc-finger; Alternative splicing.
FT ZN_FING 791 839 RING-TYPE.
FT DOMAIN 18 27 POLY-GLU.
FT VARSPPLIC 802 802 D->E (in isoform Short).
FT VARSPPLIC 803 854 /FTId=VSP_006751.
FT VARSPPLIC 803 854 Missing (in isoform Short).
FT CONFLICT 615 618 /FTId=VSP_006752.
FT CONFLICT 736 744 KOIS -> WHEG (IN REF. 2).
SQ SEQUENCE 854 AA; 98535 MW; B30F64D13208550D CRC64;

Query Match 45.5%; Score 46; DB 1; Length 854;
Best Local Similarity 47.4%; Pred. No. 31;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

RESULT 4
VG72_HSV1 STANDARD; PRT; 1350 AA.
ID VG72_HSV1
AC Q00103;
ID 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hypothetical gene 72 protein.
GN 72.
OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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OC Ictalurid Herpes-like viruses.
OX Ncbi_TaxID=10401.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Auburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
-----
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CC
DR EMBL: M75136; AAA88174.1; -.
DR PIR: G36793; G36793.
DR InterPro: IPR007087; Znf_C2H2.
DR SMART: SM00355; Znf_C2H2; 1.
KW Hypothetical protein.
SQ
SEQUENCE 1350 AA; 147547 MW; ED4780D2F290FFD CRC64;

Query Match 44.6%; Score 45; DB 1; Length 1350;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 EDVPRVPEASREBGER 20
Db :|:|:|:|:|:|
913 KSVKRIEASKEGGER 930

RESULT 5
TRPC_HALVO ID TRC_HALVO STANDARD; PRT; 251 AA.
AC P18304;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Indole-3-glycerol phosphate synthase (EC 4.1.1.48) (IGPS).
GN TRC.
OS Halobacterium volcanii (Haloflex volcanii).
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Haloflex.
OX NCB1_TaxID=2246;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370836; PubMed=2118654;
RA Lam W.L., Cohen A., Tseoluhns D.; Doolittle W.F.;
RT "Genes for tryptophan biosynthesis in the archaebacterium Haloflex
RT volcanii.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6614-6618(1990).
CC -1- CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribose 5-
CC phosphate = 1-(indol-3-yl)glycerol 3-phosphate + CO(2) + H(2)O.
CC -1- PATHWAY: Tryptophan biosynthesis; fourth step.
CC -1- SIMILARITY: BELONGS TO THE TRC FAMILY.
-----
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CC
DR EMBL: M36177; AAA72862.1; -.
DR PIR: C36044; C36044.
DR HSSP: O06121; 1A53.
DR HAMAP: MF_00134; -.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001468; IGPS.

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DR PFam; PF00218; IGPS; 1.
DR ProDom; PD001511; IGPS; 1.
DR PROSITE; PS00614; IGPS; 1.
KW Tryptophan biosynthesis; lyase; Decarboxylase.
SQ SEQUENCE 251 AA; 26754 MW; 2F2FD9E702B48065 CRC64;

Query Match 43.6%; Score 44; DB 1; Length 251;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 DVPKVEVASEREGGE 19
Db 11 DVRAILEAREPRGGE 26
|| : || || ||
|| : || || ||

RESULT 6
CREM_HUMAN
ID CREM_HUMAN STANDARD; PRT; 332 AA.
AC 003060; O16114; O16116; G9NZB9;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP responsive element modulator.
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Placenta;
RX MEDLINE=93096608; PubMed=1461747;
RA Meyer T.E., Habener J.F.;
RT "Cyclic AMP response element binding protein CREB and modulator
RT protein CREM are products of distinct genes.";
RL Nucleic Acids Res. 20:6106-6106(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=94128610; PubMed=7916662;
RA Maquiller D., Foulkes N.S., Mattei M.-G., Saessens-Corsi P.;
RT "Human CREM gene: evolutionary conservation, chromosomal localization,
RT and inducibility of the transcript.";
RL Cell Growth Differ. 4:931-937(1993).
RN [3]
RP SEQUENCE OF 1-232 FROM N.A.
RA Vouk K., Lalli B., Scherer S.W., Saessens-Corsi P., Debeljak N.,
RA Komel R., Rozman D.;
RT "Searching for mutations in the human CAMP responsive element
RT modulator (CREM) gene.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
CC SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA,
CC BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
CC TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.
CC -1- SUBUNIT: Binds DNA as a dimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Beta;
CC IsoId=Q03060-1; Sequence=displayed;
CC Name=Alpha;
CC IsoId=Q03060-2; Sequence=VSP_000599, VSP_000600, VSP_000601;
CC Name=Gamma;
CC IsoId=Q03060-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=Q03060-3; Sequence=Not described;
CC -1- PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the bZIP family.
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CC CC SYNAPSES AND CERTAIN ENDOCRINE CELL TYPES. MAY CONTROL THE
CC CC PROPERTIES OF THE MEMBRANE ASSOCIATED CYTOSKELETON.
CC CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC SURFACE OF
CC CC SYNAPTIC VESICLES.
CC CC -1- TISSUE SPECIFICITY: IS ABUNDANT IN THE FOREBRAIN AND CEREBELLUM.
CC CC IT IS ALSO FOUND IN THE ADRENAL GLAND, ANTERIOR AND POSTERIOR
CC CC PITUITARY.
CC CC -1- SIMILARITY: Contains 1 BAR domain.
CC CC -1- SIMILARITY: Contains 1 SH3 domain.
CC CC
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: X60422; CAA42953.1; -.
CC CC
CC CC PIR: S22700; S22700.
CC CC
CC CC InterPro: IPR003005; Amphiphysin.
CC CC InterPro: IPR003017; Amphiphysin_1.
CC CC InterPro: IPR006632; BAR.
CC CC InterPro: IPR004148; BAR_dom.
CC CC InterPro: IPR001452; SH3.
CC CC
CC CC Pfam: PF03114; BAR; 1.
CC CC Pfam: PF00018; SH3; 1.
CC CC
CC CC PRINTS: PRO1251; AMPHIPHYNSIN.
CC CC PRINTS: PRO0452; SH3DOMAIN.
CC CC ProDom: PD003208; Amphiphysin_1; 1.
CC CC ProDom: PD000066; SH3; 1.
CC CC
CC CC SMART: SM00721; BAR; 1.
CC CC SMART: SM00326; SH3; 1.
CC CC PROSITE: PS50002; SH3; 1.
CC CC
CC CC Cysoskeleton; SH3 domain; Coiled coil.
CC CC
CC CC DOMAIN 10 84 COILED COIL (POTENTIAL).
CC CC DOMAIN 144 191 COILED COIL (POTENTIAL).
CC CC DOMAIN 609 682 SH3.
CC CC
CC CC SEQUENCE 682 AA; 75205 MW; 61617F94F38BE20 CRC64;
CC CC
QY Query Match 43.6%; Score 44; DB 1; Length 682;
Db Best Local Similarity 57.1%; Pred. No. 49;
Matches 12; Conservative 2; Mismatches 5; Indels 2; Gaps 2;
QY 1 EVEDPKVY-EPASREG-GE 19
Db 529 KVSSIPSVVIEPASNBEGE 549

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RT		"Complete genome sequence of Methanobacterium thermoautotrophicum
RJ		deltah; functional analysis and comparative genomes.";
RL	J. Bacteriol.	179:7135-7155(1997).
CC	-I - CATALYTIC ACTIVITY:	ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC	+ L-valyl-tRNA(Val)].	
CC	-I - SUBCELLULAR LOCATION:	Cytoplasmic.
CC	-I - SIMILARITY:	Belongs to class-I aminoacyl-tRNA synthetase family.
CC		-----
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CC		-----
DR	EMBL; AB000855; AAB85270.1; .-	
DR	HSSP; P96142; IGAX.	
DR	InterPro; IPR002300; CRNA-synt_1a.	
DR	InterPro; IPR001412; CRNA-synt_I.	
DR	InterPro; IPR002303; CRNA-synt_val.	
DR	Pfam; PF00133; CRNA-synt_1; 1.	
DR	PRINTS; PR00986; TRNASYNTHAL.	
DR	TIGRFAMs; TIGR00422; vals; 1.	
DR	PROSITE; PS00178; AA-TRNA_Ligase_I; 1.	
KW	Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;	
KW	Complete proteome.	
FT	SITE	46
FT	SITE	529
FT	BINDING	532
SO	SEQUENCE	877 AA; 100946 MW; B935720D6BFFDB CRC64;
		"HIGH" REGION.
		"KMSKS" REGION.
		ATP (BY SIMILARITY).

```

Query Match      43.6%; Score 44; DB 1; Length 877;
Best Local Similarity 46.7%; Pred No: 64;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps

QY      3 EDVPKVVEPASEREG 17
      |:::|::|
DB      709 EHIPEIVDPERSG 723

RESULT 10
PCH7 HUMAN STANDARD; PRT; 1069 AA.
AC 060245: 060246: 060247:
AT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DS Protocadherin 7 precursor [Brain-heart protocadherin] (BH-Pcdh).
GN PCP7 OR BHPCDH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A, B AND C).
RX MEDLINE=98277460; PubMed=9615233;
RA Yoshida K., Yoshimoto-Nakagawa K., Seki N., Sasaki M., Sugano S.;
RT "Cloning, expression analysis, and chromosomal localization of
RT BH-protocadherin (PCP7)", a novel member of the cadherin
RT superfamily."
RL Genomics 49:458-461(1998).
RC -1 SUBCELLULAR LOCATION: Type I membrane protein.
CC -1 ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=3;
CC Name=A; Synonyms=BH-Pcdh-a;
CC IsoId=O60245-1; Sequence=Displayed;
CC Name=B; Synonyms=BH-Pcdh-b;
CC IsoId=O60245-2; Sequence=VSP_000704;
CC Name=C; Synonyms=BH-Pcdh-c;
CC IsoId=O60245-3; Sequence=VSP_000705, VSP_000706,
CC -1 TISSUE SPECIFICITY: Expressed predominantly in brain and heart and
CC at lower levels in various other tissues.

```

DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	DNA (cytosine-5'-methyltransferase 1 (BC 2.1.1.37) (Dnm1l) (DNA
DE	methyltransferase Ggal) (DNA Mrase Ggal) (MCMT) (M.ggal).
GN	DNM1T OR DNM1T OR AIM.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
OX	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96172572; Pubmed=8586618;
RA	Tajima S., Tsuda H., Wakabayashi N., Aaso A., Mizuno S.,
RA	Mishimori K.;
RT	"Isolation and expression of a chicken DNA methyltransferase cDNA,"
RL	J. Biochem. 117:1050-1057(1995).
RL	[2]
RL	INTERACTION WITH PCNA, AND MUTAGENESIS OF VAL-190.
RP	MEDLINE=97451025; Pubmed=9302295;
RX	Chuang L.S.-H., Ian H.-I., Koh T.-W., Ng H.-H., Xu G., Li B.F.L.;
RA	"Human DNA-(cytosine-5' methyltransferase-PCNA complex as a target for
RT	p21WAF1,"
RL	Science 277:1996-2000(1997).
CC	-1- FUNCTION: Methylates CpG residues. Preferentially methylates
CC	hemimethylated DNA. It is responsible for maintaining methylation
CC	patterns established in development (By similarity) Mediates
CC	transcriptional repression by direct binding to HDAC2 (By
CC	similarity)
CC	-1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
CC	homocysteine + DNA containing 5-methylcytosine.
CC	-1- SUBUNIT: Interacts with PCNA.
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC	-1- TISSUE SPECIFICITY: Testis and lung.
CC	-1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
CC	-1- SIMILARITY: Contains 2 BAH domains.
CC	-1- SIMILARITY: Contains 1 CXXC-type zinc finger.
CC	-----
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CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; DA3920; BAA07867.1; -
DR	PIR; JC4172; JC4172.
DR	REBASE; 3020; M.Ggal.
DR	InterPro; IPR001025; BAH.
DR	InterPro; IPR001525; C5_DNA_meth.
DR	InterPro; IPR002857; Znf_CXXC.
DR	Pfam; PF014426; BAH; 2.
DR	Pfam; PF00145; DNA_methylase; 1.
DR	Pfam; PF02008; zf-CXXC; 1.
DR	PRINTS; PR00105; CSMETTFPASE.
DR	SMART; SMO0439; BAH; 2.
DR	TIGRFAMs; TIGR00675; dcm; 1.
DR	PROSITE; PS00094; C5_MTASE_1; 1.
DR	PROSITE; PS00095; C5_MTASE_2; 1.
KW	Transferase; Methyltransferase; Transcription regulation; Repressor;
KW	DNA-binding; Zinc-finger; Zinc; Metal-binding; Nuclear protein;
KW	Repeat; Phosphorylation.
FT	DOMAIN 182 194
FT	ZN_FING 557 603
FT	DOMAIN 667 791
FT	DOMAIN 877 1011
FT	DOMAIN 1020 1034
FT	DOMAIN 129 149
FT	DOMAIN 217 227
FT	MOD_RES 420 420
FT	ACT_SITE 1141 1141
FT	ACG_SITE 1141 1141
FT	BY SIMILARITY.
FT	INTERACTS WITH PCNA.
FT	CXXC-TYPE.
FT	BAH 1.
FT	BAH 2.
FT	7.5 X 2 AA TANDEM REPEATS OF K-G.
FT	POLY-SER.
FT	POLY-GLU.
FT	PHOSPHORYLATION (BY SIMILARITY).
FT	BY SIMILARITY.

FT MUTAGEN 190 190 V->H: NO LOSS OF INTERACTION WITH PCNA.
SQ SEQUENCE 1537 AA; 172906 MW; FB7E0B2CD10EA17E CRC64;
Query Match 43.6%; Score 44; DB 1; Length 1537;
Best Local Similarity 46.7%; Pred. No. 11e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
OY 3 EDVKEVPEASEREG 17
:::|||||
Db 816 KEIPKVAEPDREGDG 830
RESULT 12
APC_RAT STANDARD; PRT; 2842 AA.
ID APC_RAT
AC P70378;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Adenomatous polyposis coli protein (APC protein).
GN APC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344/N; TISSUE=Brain;
RX MEDLINE=96116966; PubMed=8563176;
RA Toyota M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A.,
RA Sugimura T., Nago M.;
RT "cDNA cloning of the rat APC gene and assignment to chromosome 18.";
RL Mamm. Genome 6:746-748(1995).
RN [2]
RP MUTAGENESIS.
RC STRAIN=Sprague-Dawley, and Fischer 344/N;
RX MEDLINE=95148647; PubMed=7846077;
RA Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
RA Weisburger J.H., Sugimura T., Nago M.;
RT "Specific 5'-GCCG-3'--5'-GCA-3' mutation of the APC gene in rat colon
tumors induced by 2-amino-1-methyl-6-phenylimidazo(4,5-b)pyridine.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
CC -1- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1
and participates in Wnt signaling. APC activity is correlated with
its phosphorylation state (By similarity).
CC -1- SUBUNIT: Forms homooligomers. Associates with catenins. Binds
axin (By similarity).
CC -1- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
CC -1- SIMILARITY: Contains 7 ARM repeats.
CC -----
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CC -----
CC EMBL; D38629; BA007609.1; -.
DR HSSP; Q02248; 3BCT.
DR InterPro; IPR000225; Armadillo.
DR Pfam; PF00514; Armadillo_seg; 4.
DR SMART; SMO0185; ARM; 5.
DR PROSITE; PS0076; ARM_REPEAT; 1.
KW Wnt signaling pathway; Anti-oncogene; Phosphorylation; Coiled coil;
Repeat.
KW DOMAIN 1 728 LEU-RICH.
FT DOMAIN 1 62 COILED COIL (POTENTIAL).
FT DOMAIN 125 260 COILED COIL (POTENTIAL).
FT REPEAT 451 493 ARM 1.
FT REPEAT 503 545 ARM 2.
FT REPEAT 546 589 ARM 3.
FT REPEAT 590 636 ARM 4.

FT REPEAT 637 681 ARM 5.
FT REPEAT 682 723 ARM 6.
FT REPEAT 724 765 ARM 7.
FT DOMAIN 739 2831 SER-RICH.
FT DOMAIN 1130 1155 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).
FT MUTAGEN 1864 1891 HIGHLY CHARGED.
SQ SEQUENCE 2842 AA; 310530 MW; 3CB2EA8A34B8F47 CRC64;
Query Match 43.1%; Score 43.5; DB 1; Length 2842;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
OY 4 DVPEVPEASE-REGGER 20
:::|||||
Db 1450 EVPTKVPALAEKREGPK 1467
RESULT 13
CREM_MOUSE STANDARD; PRT; 341 AA.
ID CREM_MOUSE
AC P27699; P27698;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP responsive element modulator.
GN CREM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA, BETA AND GAMMA).
RX MEDLINE=91145994; PubMed=1847666;
RA Foulkes N.S., Borrelli E., Sassone-Corsi P.;
RT "CREM gene: use of alternative DNA-binding domains generates multiple
antagonists of CAMP-induced transcription.";
RL Cell 64:739-749(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM TAU).
RX MEDLINE=92119336; PubMed=1370576;
RA Foulkes N.S., Mellstrom B., Benuiglio E., Sassone-Corsi P.;
RT "Developmental switch of CREM function during spermatogenesis: from
antagonist to activator.";
RL Nature 355:80-84(1992).
CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. ISOFORMS
ALPHA, BETA, AND GAMMA ARE ANTAGONISTS OF THE CAMP TRANSCRIPTIONAL
RESPONSE, WHILE ISOFORM TAU IS AN ACTIVATOR.
CC -1- SUBUNIT: Binds DNA as a dimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Tau;
CC IsoId=P27699-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P27699-2; Sequence=VSP_000602, VSP_000603, VSP_000604,
CC VSP_000607;
CC Name=Beta;
CC IsoId=P27699-3; Sequence=VSP_000602, VSP_000603, VSP_000604;
CC Name=Gamma;
CC IsoId=P27699-4; Sequence=VSP_000602, VSP_000605, VSP_000606;
CC -1- DEVELOPMENTAL STAGE: IN PREMITOTIC GERM CELLS, EXPRESSED AT LOW
AMOUNTS IN THE ANTAGONIST FORM. SUBSEQUENTLY, DURING
SPERMATOGENESIS, THE ISOFORM TAU (ACTIVATOR) IS GENERATED
EXCLUSIVELY AND IN EXTREMELY HIGH AMOUNT.
CC -1- PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the bZIP family.
CC -----
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GN PRFB OR CGL0801.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteriales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxId=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Peptide chain release factor 2 directs the termination
CC of translation in response to the peptide chain termination codons
CC UGA and UAA (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE
CC FACTORS FAMILY.
CC -----
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CC -----
CC EMBL; AP005276; BAB98194.1; -
CC HAMAP; MF_00094; -; 1.
CC InterPro; IPR005139; PCRF.
CC InterPro; IPR000352; Pep_rel_factor_1.
CC InterPro; IPR004374; PRFB.
CC Pfam; PF03462; PCRF; 1.
CC Pfam; PF00472; RF-1; 1.
CC TIGRFAMs; TIGR00020; prfb; 1.
CC PROSITE; PS00745; RF_PROK_1; 1.
CC Protein biosynthesis; Complete proteome.
CC *KW SEQUENCE 368 AA; 41137 MW; C94D86D050AC5230 CRC64;
CC SQ

```

Query Match 42.6%; Score 43; DB 1; Length 368;

Best Local Similarity 50.0%; Pred. No. 37;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 2 VEDVKKVVEPASEREK 17
 :||:|||||:
 Db 75 IEDLPIMVELAEBEDG 90

Search completed: August 1, 2003, 18:27:43
 Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2003, 18:27:50 ; Search time 39 seconds
(without alignments)
49.317 Million cell updates/sec

Title: US-10-017-168-15
Perfect score: 101
Sequence: 1 EVEDVPKVEBPASREGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	97	96.0	256	2	F71326 hypothetical prote
2	82	81.2	227	2	G71326 hypothetical prote
3	51.5	51.0	153	1	B69215 conserved hypothet
4	50	49.5	184	2	D84603 hypothetical prote
5	48	47.5	547	2	E70650 phosphoglucomutase
6	47	46.5	308	2	T17946 hypothetical prote
7	47	46.5	1151	2	T24541 hypothetical prote
8	46.5	46.0	946	2	D66503 protein PG16.9 (i
9	46	45.5	437	2	C35147 integrase homolog
10	45	44.6	99	2	A55819 nonhistone chromos
11	45	44.6	178	2	B95994 hypothetical prote
12	45	44.6	264	1	G69884 conserved hypothet
13	45	44.6	798	2	T33022 hypothetical prote
14	45	44.6	873	2	T16282 hypothetical prote
15	45	44.6	1350	2	G36793 hypothetical prote
16	44	43.6	220	1	C36044 CAMP response elem
17	44	43.6	251	1	C36044 insole-3-glycerol-
18	44	43.6	306	2	T00177 hypothetical prote
19	44	43.6	306	2	G89888 hypothetical prote
20	44	43.6	344	2	JC5601 CAMP response elem
21	44	43.6	681	2	JC5602 probable transpos
22	44	43.6	681	2	B81815 amphihsyn - chic
23	44	43.6	892	1	S22700 valine-tRNA ligase
24	44	43.6	897	2	E69202 BH:protocadherin-a
25	44	43.6	1069	2	T00043 BH:protocadherin p
26	44	43.6	1072	2	T00041 BH:protocadherin p
27	44	43.6	1200	2	T00042 BH:protocadherin p
28	44	43.6	1537	2	JC4172 DNA (cytosine-5-)-
29	43	42.6	133	2	T36525 hypothetical prote

30	43	42.6	199	2	AB2847 conserved hypothet
31	43	42.6	210	2	CB7305 hypothetical prote
32	43	42.6	217	2	C37944 CAMP response elem
33	43	42.6	220	2	A75287 response regulator
34	43	42.6	227	2	B97624 hypothetical prote
35	43	42.6	229	2	B37944 CAMP response elem
36	43	42.6	229	2	A37944 CAMP response elem
37	43	42.6	278	2	S36101 CAMP response elem
38	43	42.6	341	2	S20827 CAMP response elem
39	43	42.6	341	2	S26686 CAMP response elem
40	43	42.6	356	2	B71023 hypothetical prote
41	43	42.6	369	2	A39157 probable RNA helic
42	43	42.6	434	2	T47545 monodehydroascorba
43	43	42.6	542	2	E84250 acetyl-CoA synthet
44	43	42.6	668	1	Q08EW1 U52 protein - hum
45	43	42.6	670	1	YCMU acetoacetate synth

ALIGNMENTS

RESULT 1
F71326
hypothetical protein TP0433 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: F71326
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uitterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A11250; MUID:98332770; PMID:9665876
A:Accession: F71326
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-256 <COL>
A:Cross-references: GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AC65421.1; PID:G332271
A:Experimental source: errain Nichols
C:Genetics:
A:Gene: TP0433

Query Match
Best Local Similarity 96.0%; Score 97; DB 2; Length 256;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVEDVPKVEBPASREGER 20
Db 184 EVEDVPKVEBPASREGER 203

RESULT 2
G71326
hypothetical protein TP0434 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: G71326
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uitterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A11250; MUID:98332770; PMID:9665876
A:Accession: G71326
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-227 <COL>
A:Cross-references: GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AC65422.1; PID:G332271
A:Experimental source: errain Nichols
C:Genetics:
A:Gene: TP0434

Query Match
Best Local Similarity 81.2%; Score 82; DB 2; Length 227;

C:Genetics:
A:Gene: CESP:T05F1.6a
A:Map position: 1
A:Introns: 9/1; 21/2; 43/3; 186/3; 483/2; 574/3; 611/1; 957/3; 1029/2; 1124/3

Query Match 46.5%; Score 47; DB 2; Length 1151;
Best Local Similarity 45.0%; Pred. No. 64;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

OY 1 EVEDVPKVEPASEREGGER 20
DB 659 EMEADPATATTPASNRKRKR 678

RESULT 8

D96503
protein P9C16.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96503
R:Theologian, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: D96503
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-946 <STO>
A:Cross-references: GB:AEO05173; NID:98778679; PIDN:AAF9687.1; GSPDB:GN00141
C:Genetics:
A:Gene: P9C16.9
A:Map position: 1

Query Match 46.0%; Score 46.5; DB 2; Length 946;
Best Local Similarity 47.8%; Pred. No. 63;
Matches 11; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

OY 1 EVEDVPK--VEPASEREGGER 20
DB 24 EADVPQVVDVQPKSNKSRKR 46

RESULT 9

C35147
integrase homolog - Saccharopolyspora erythraea
C:Species: Saccharopolyspora erythraea
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 22-Oct-1999
C:Accession: C35147
R:Brown, D.P.; Idler, K.B.; Katz, L.
J. Bacteriol. 172, 1877-1888, 1990
A:Title: Characterization of the genetic elements required for site-specific integration
A:Reference number: A35147; MUID:90202705; PMID:2180909
A:Accession: C35147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-437

A:Cross-references: GB:M35138; NID:9152671; PIDN:AA98345.1; PID:9152674

Query Match 45.5%; Score 46; DB 2; Length 437;
Best Local Similarity 50.0%; Pred. No. 33;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 EVEDVPKVEPASEREGGER 20
DB 185 EVEDMQLVIAKALERRNGVR 204

RESULT 10
A55819
nonhistone chromosomal protein CHMG-I - midge (Chironomus tentans)

M:Alternate names: high mobility group protein I/Y homolog
C:Species: Chironomus tentans
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 21-Jul-2000
C:Accession: A55819; S47253; S47252
R:Claus, P.; Schulze, E.; Wisniewski, J.R.
J. Biol. Chem. 269, 33042-33048, 1994

A:Title: Insect proteins homologous to mammalian high mobility group proteins I/Y (HMG I
A:Reference number: A55819; MUID:95105193; PMID:7806532
A:Accession: A55819
A:Molecule type: mRNA
A:Residues: 1-99 <CLA>

A:Cross-references: EMBL:Z36898; NID:9534932; PIDN:CAA65365.1; PID:9534933
A:Experimental source: clone pCM126
R:Claus, P.; Schulze, E.; Wisniewski, J.R.
submitted to the EMBL Data Library, August 1994

A:Description: Insect proteins homologous to mammalian high mobility group proteins I/Y
A:Reference number: S47252
A:Accession: S47253
A:Molecule type: DNA

A:Residues: 1-91, 'A', '93-99 <CL2>
A:Cross-references: EMBL:Z36897; NID:9534886; PID:9534887
A:Experimental source: clone pCWG106
C:Genetics:

A:Introns: 15/3; 76/1
A>Note: suggested by Southern blot analysis in Ref A55819 to be single copy gene
C:Keywords: chromosomal protein; DNA binding
F:8-13/Region: DNA-binding motif (K/R-G-R-G-R-P)
F:55-60/Region: DNA-binding motif (K/R-G-R-G-R-P)
F:75-80/Region: DNA-binding motif (K/R-G-R-G-R-P)

Query Match 44.6%; Score 45; DB 2; Length 99;
Best Local Similarity 44.4%; Pred. No. 10;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 EVEDVPKVEPASEREGG 18
DB 33 KVEEVPKKEESTKPEENG 50

RESULT 11

E95994
hypotheoretical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplaemid pSymb
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: E95994
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Herman
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,663-kb pSymb magaplaemid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11461431
A:Accession: E95994
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-178 <KIR>
A:Cross-references: GB:A5591985; PIDN:CAC49621.1; PID:915141108; GSPDB:GN00167
A:Experimental source: strain 1021, magaplaemid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaulic, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:

A:Gene: Smb21395
A:Genome: plasmid

Query Match 44.6%; Score 45; DB 2; Length 178;

Best Local Similarity	41.2%;	Pred. No. 19;			
Matches	7; Conservative	4; Mismatches	6; Indels	0; Gaps	0;

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QY      2 VEDVPKVEPASEREGG 18
        :|:|:|:|:|
Db     157 IPIPTLAEPEDQPEGG 173
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RESULT 12
G69884

conserved hypothetical protein ymdB - *Bacillus subtilis*
C:Species: *Bacillus subtilis*

C: Update: 10-Sep-1999 #sequence_rev: 10-Sep-1999 #text_change: 21-Jul-2000
C: Accession: G69884
D: Keyword: B. Cereus, N. Weger, T. Albert, J. M. Allen, C. Brown, H. Dubois
E: Description: B. Cereus, N. Weger, T. Albert, J. M. Allen, C. Brown, H. Dubois

A., Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E. *Nature* 390, 249-256, 1997

A:Authors: Fougere, D.; Frit, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gallen, J.; Harwood, C.R.; Henaut, A.; Hiltbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Iech, J.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinios, P.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, A.

Y. M., Udagawa, M., Ugiwara, A., Udagawa, B., Park, S.H., Parro, V., Pohl, I.M., Portetelli, R., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadle, Y., Sato, T., Scanlon, T., Schleich, S., Schroeder, R., Scifone, F., Sekiguchi, J., Sekowa, A., Serocino, A., Akeuchi, M., Tamakoshi, A., Tanaka, T., Terpetra, P., Tognoni, A., Tosato, V., Uchiyama,

A:Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: G69884
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-264 <KDN>

A/Cross-References: GB:Z59112; GB:AL00126; NID:g2633902; PIDN:CAB13570.1; PID:g2634069
A/Experimental source: strain 168
C/Genetics:
A/Gene: ymcb

c/superfamily: hypotnetical protein ymdB

Query Match	44.6%	Score 45;	DB 1;	Length 264;
Best Local Similarity	50.0%	Pred. No. 28;		

Matches	8;	Conservative	4;	Mismatches	4;	Indels	0;	Gaps	0;
QY	2	VEDVPKVVPEASEREQ	17						
	::: : : : :								

Db	79	IDDV/PNLV/RP/ANFPEG	94
RESULT 13			

T33022
hypothetical protein K07H8.10 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
#Date: 29-Oct-1999 #sequence revision 29-Oct-1999 #text change 29-Oct-1999

C;Accession: T33022
R;Fulton, B.; Hawkins, J.; Gattung, S.; Wohlmann, P.; Elliott, G.
submitted to the EMBL Data Library, February 1998
.;Description: The sequence of *C. elegans* cosmid K07H8.

A:Reference number: Z21264
A:Accession: T33022
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-798 <Full>
A:Cross-references: EMBL:AF047659; PIDN:AAC04430.1; GSPDB:GN00022; CESP:K07H8.10
A:Experimental source: strain Bristol N2; clone K07H8
A:Genetics:

A₁Gene: CESP:K07H8.10
A₁Map position: 4
A₁Introns: 205/1; 308/3; 630/1; 773/3

Query March	44.6%	Score 45;	DB 2;	Length 798;
Best local Similarity	44.4%	Pred. No. 89;		
Matches	8;	Conservative	4;	Mismatches 6; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 1, 2003, 18:37:21 ; Search time 21 Seconds
(without alignments)
113.105 Million cell updates/sec

Title: US-10-017-168-15
Perfect score: 101
Sequence: 1 EVEDPKVEPASEREGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	48.5	266	US-10-036-542-66	Sequence 66, App1
2	49	48.5	277	US-10-036-542-92	Sequence 92, App1
3	49	48.5	277	US-10-036-542-134	Sequence 134, App1
4	49	48.5	288	US-10-036-542-130	Sequence 130, App1
5	49	48.5	304	US-09-925-300-1615	Sequence 1615, App1
6	44	43.6	71	US-09-864-761-35920	Sequence 35920, App1
7	44	43.6	268	US-09-764-864-11772	Sequence 11772, App1
8	44	43.6	392	US-10-156-761-10989	Sequence 10989, App1
9	44	43.6	1038	US-09-752-639-151	Sequence 151, App1
10	44	43.6	1038	US-09-984-198-151	Sequence 151, App1
11	43	42.6	57	US-10-211-088-109	Sequence 109, App1
12	43	42.6	178	US-09-764-864-1091	Sequence 1091, App1
13	43	42.6	241	US-09-738-626-6590	Sequence 6590, App1
14	43	42.6	266	US-10-102-806-605	Sequence 605, App1
15	43	42.6	368	US-09-738-626-4393	Sequence 4393, App1

16	43	42.6	670	US-10-057-609B-3	Sequence 3, App1
17	43	42.6	670	US-10-004-827-3	Sequence 4, App1
18	43	42.6	670	US-10-004-827-4	Sequence 4, App1
19	43	42.6	670	US-10-004-827-26	Sequence 26, App1
20	43	42.6	811	US-09-840-787-45	Sequence 45, App1
21	42	41.6	295	US-09-975-719-341	Sequence 341, App1
22	41.5	41.1	554	US-09-815-242-5728	Sequence 5728, App1
23	41.5	41.1	1592	US-09-815-242-12160	Sequence 12160, App1
24	41.5	41.1	1592	US-09-832-292-35	Sequence 35, App1
25	41	40.6	249	US-09-815-242-11658	Sequence 11658, App1
26	41	40.6	285	US-10-156-761-13708	Sequence 13708, App1
27	41	40.6	554	US-09-746-491-41	Sequence 41, App1
28	41	40.6	749	US-10-211-962-98	Sequence 98, App1
29	41	40.6	1106	US-10-157-331-30	Sequence 30, App1
30	41	40.6	5215	US-09-861-289-2	Sequence 2, App1
31	41	40.6	5215	US-09-860-446-2	Sequence 2, App1
32	41	40.6	5215	US-09-988-384B-2	Sequence 2, App1
33	41	40.6	5215	US-09-836-821-2	Sequence 2, App1
34	40.5	40.1	59	US-09-967-237-50	Sequence 50, App1
35	40.5	40.1	98	US-09-772-719-50	Sequence 50, App1
36	40.5	40.1	377	US-09-967-237-87	Sequence 87, App1
37	40.5	40.1	459	US-09-772-719-2	Sequence 2, App1
38	40.5	40.1	459	US-09-967-237-2	Sequence 2, App1
39	40.5	40.1	610	US-09-783-708-1	Sequence 1, App1
40	40	39.6	26	US-09-864-761-38892	Sequence 38892, App1
41	40	39.6	114	US-09-796-692-2447	Sequence 2447, App1
42	40	39.6	114	US-10-040-862-2447	Sequence 2447, App1
43	40	39.6	315	US-10-245-107-44	Sequence 44, App1
44	40	39.6	315	US-10-245-107-44	Sequence 44, App1
45	40	39.6	315	US-10-245-143-44	Sequence 44, App1

ALIGNMENTS

RESULT 1
US-10-036-542-66
; Sequence 66, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Bire et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: P0402P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-66

Query Match 48.5%; Score 49; DB 15; Length 266;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 DVKVEPASEREGG 18
DB 238 BIPVFDEKERESG 252

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RESULT 2
US-10-036-542-92
; Sequence 92, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birste et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 92
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-036-542-92

Query Match      48.5%; Score 49; DB 15; Length 277;
Best Local Similarity 53.3%; Pred. No. 13;
Matches      8; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY      4 DVPKVEPASEREGG 18
Db      238 EIKPVDPKEREESG 252

RESULT 3
US-10-036-542-134
; Sequence 134, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birste et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 134
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-036-542-134

Query Match      48.5%; Score 49; DB 15; Length 277;
Best Local Similarity 53.3%; Pred. No. 13;
Matches      8; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY      4 DVPKVEPASEREGG 18
Db      238 EIKPVDPKEREESG 252

RESULT 4
US-10-036-542-130
; Sequence 130, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birste et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 130
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-130

Query Match      48.5%; Score 49; DB 15; Length 288;
Best Local Similarity 53.3%; Pred. No. 13;
Matches      8; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY      4 DVPKVEPASEREGG 18
Db      261 EIKPVDPKEREESG 275

RESULT 5
US-09-925-300-1615
; Sequence 1615, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1615
; LENGTH: 304
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1615

Query Match
Best Local Similarity 48.5%; Score 49; DB 10; Length 304;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 DVPKVVPEASEREKG 18
Db 265 EIPKVFDEKERESG 279

RESULT 6
US-09-864-761-35920
; Sequence 35920, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35920
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: MAP TO AC006146.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EST_HUMAN HIT: A1702990.1, EVALU8 7.20e-02
US-09-864-761-35920

Query Match
Best Local Similarity 43.6%; Score 44; DB 9; Length 71;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 EDVPKVVPEASEREGER 20
Db 185 EBPVPEIQEKQEBGRER 202

RESULT 7
US-09-764-864-1172
; Sequence 1172, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1172
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (261)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (1262)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1172

Query Match
Best Local Similarity 43.6%; Score 44; DB 10; Length 268;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 EDVPKVVPEASEREGER 20
Db 185 EBPVPEIQEKQEBGRER 202

RESULT 8
US-10-156-761-10989
; Sequence 10989, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATORI, MASAHIRA
```

;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-262
;; CURRENT APPLICATION NUMBER: US/10/156,761
;; CURRENT FILING DATE: 2002-05-29
;; PRIOR APPLICATION NUMBER: JP 2001-204089
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO 10989
;; LENGTH: 392
;; TYPE: PRT
;; ORGANISM: Streptomyces avermitilis
US-10-156-761-10989

Query Match
Best Local Similarity 43.6%; Score 44; DB 15; Length 392;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 EVEDVPKVEPASEEGE 19
|||:|:|:|:|:
Db 23 EVIDTPEAREATERLGK 41

RESULT 9
US-09-752-639-151
; Sequence 151, Application US/09752639
; Patent No. US20020091243A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: PasteSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;; TOPOLOGY: linear
US-09-752-639-151

Query Match
Best Local Similarity 43.6%; Score 44; DB 9; Length 1038;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 EDVPKVEPASEEGE 20
|||:|:|:|:|:
Db 954 EVDPEIQEKKEQEGRR 971

RESULT 10
US-09-984-198-151
; Sequence 151, Application US/09984198
; Patent No. US20020106679A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: PasteSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,198
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-984-198-151

Query Match
Best Local Similarity 43.6%; Score 44; DB 10; Length 1038;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 EDVPKVEPASEEGE 20
|||:|:|:|:|:
Db 954 EVDPEIQEKKEQEGRR 971

```

RESULT 11
US-10-211-088-109
; Sequence 109, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: NO. US20030104479A1 Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13.
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-109

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Query Match	42.6%	Score 43	DB 15	Length 57
Best Local Similarity	47.1%	Pred. No. 17		
Matches	8	Conservative	3	Mismatches 6; Indels 0; Gaps 0
Qy	1	EVEDYKVVPEASEREG	17	
	:	: : : : : :		
Db	39	DVPGIPKIEEKSEEEG	55	

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RESULT 12
US-09-764-864-1091
: Sequence 1091, Application US/09764864
: Patent No. US20020132753A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT23
: CURRENT APPLICATION NUMBER: US/09/764,864
: PRIORITY FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 1792
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1091
: LENGTH: 178
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-764-864-1091

```

Query Match	42.6%	Score	43	DB	10	Length	178
Best Local Similarity	53.3%	Pred	No. 62				
Matches	8	Conservative	3	Mismatches	4	Indels	0
				Gaps			0

```
QY      6 PKVPEASEREGGER 20
          |::|||
Db     129 PRLSVPAAPREGGAR 143
```

RESULT 13
US-09-738-626-6590
; Sequence 6550, Application US/0973862626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIHO

```

1  APPLICANT: YOKOJI HARUHIKO
2  APPLICANT: TATEISHI, NAOKO
3  APPLICANT: SENOH, AKIHIRO
4  APPLICANT: IKEDA, MASATO
5  APPLICANT: OZAKI, AKIO
6  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
7  FILE REFERENCE: 249-125
8  CURRENT APPLICATION NUMBER: US/09/738,626
9  PRIOR FILING DATE: 2000-12-18
10 PRIOR APPLICATION NUMBER: JP 99/377484
11 PRIOR FILING DATE: 1999-12-16
12 PRIOR APPLICATION NUMBER: JP 00/159162
13 PRIOR FILING DATE: 2000-04-07
14 PRIOR APPLICATION NUMBER: JP 00/280988
15 PRIOR FILING DATE: 2000-08-03
16 NUMBER OF SEQ ID NOS: 7059
17 SOFTWARE: PatentIn ver. 3.0
18 SEQ ID NO 6530
19 LENGTH: 241
20 TYPE: prt
21 ORGANISM: Corynebacterium glutamicum
22 US-09-738-626-6590

```

Query Match	42.6%	Score 43;	DB 10;	Length 241;
Best Local Similarity	56.2%	Pred. No. 87;		
Matches	9;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0;

QY 4 DVPKVEPASEREGB 19
|||:|:|:|
Db 78 DVPEAVKDASEKYGE 93

```

RESULT 14
US-10-102-806-605
: Sequence 605, Application US/10102806
: Publication No. US20030054421A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA103PIC1
: CURRENT APPLICATION NUMBER: US/10/102,806
: CURRENT FILING DATE: 2002-03-22
: PRIOR APPLICATION NUMBER: 09/925,298
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05881
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 846
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 605
: LENGTH: 266
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (84)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-605

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Query	March	42.6%	Score 43	DB 15	Length 266
	Best Local Similarity	56.2%	Pred. No. 97		
Matches	9	Conservative	2	Mismatches	5
				Indels	0
				Gaps	0
QY	3	EDVPRVYEPASEREBCG	18		
Db	140	EDNEVVRPHNGRVGG	155		

RESULT 15
US-09-738-626-4393
; Sequence 4393, Application US/09738626
; Publication No. US20020197605A1

```
/ GENERAL INFORMATION:
/ APPLICANT: NAKAGAWA, SATOSHI
/ APPLICANT: MIZOGUCHI, HIROSHI
/ APPLICANT: ANDO, SEIKO
/ APPLICANT: HAYASHI, MIKIRO
/ APPLICANT: OCHIAI, KEIKO
/ APPLICANT: YOKOI, HARUHIKO
/ APPLICANT: TATEISHI, NAKO
/ APPLICANT: SENOH, AKIHIRO
/ APPLICANT: IKEDA, MASATO
/ APPLICANT: OZAKI, AKIO
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-125
/ CURRENT APPLICATION NUMBER: US/09/738,626
/ CURRENT FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: JP 99/377484
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: JP 00/159162
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: JP 00/280988
/ PRIOR FILING DATE: 2000-08-03
/ NUMBER OF SEQ ID NOS: 7059
/ SOFTWARE: PatentIn ver. 3.0
/ SEQ ID NO 4393
/ LENGTH: 368
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-09-738-626-4393

Query Match      42.6%; Score 43; DB 10; Length 368;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      2 VEDVPRKVEPAPSEREG 17
Db      75 IEDLPIMVELAEEDG 90
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Search completed: August 1, 2003, 18:45:48
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2003, 18:34:15 ; Search time 29 seconds
(without alignments)
29.180 Million cell updates/sec

Title: US-10-017-168-15
Perfect score: 101
Sequence: 1 EVEDPKVPEPAREGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47.5	47.0	801	US-09-134-001C-5584	Sequence 5584, Ap
2	47	46.5	117	US-09-163-748C-7	Sequence 7, Appl
3	46.5	46.0	571	US-09-252-991A-26148	Sequence 26148, A
4	44	43.6	228	US-09-252-991A-32898	Sequence 32898, A
5	44	43.6	747	US-09-035-648-18	Sequence 18, Appl
6	44	43.6	747	US-09-001-951-18	Sequence 18, Appl
7	44	43.6	747	US-08-818-829-18	Sequence 18, Appl
8	43	42.6	670	US-08-363-208-2	Sequence 2, Appl
9	43	42.6	671	US-09-137-478-2	Sequence 2, Appl
10	43	42.6	671	US-08-426-125-8	Sequence 8, Appl
11	43	42.6	671	US-08-455-355-8	Sequence 8, Appl
12	43	42.6	671	US-09-367-512-7	Sequence 7, Appl
13	43	42.6	761	US-09-046-894-35	Sequence 35, Appl
14	43	42.6	811	US-08-933-750C-45	Sequence 45, Appl
15	43	42.6	811	US-09-234-613-45	Sequence 45, Appl
16	43	42.6	1805	US-07-853-913-2	Sequence 2, Appl
17	42	41.6	151	US-09-732-210-1401	Sequence 1401, Ap
18	42	41.6	295	US-09-199-637A-341	Sequence 341, App
19	42	41.6	346	US-09-252-991A-21487	Sequence 21487, A
20	42	41.6	461	US-09-252-991A-32102	Sequence 32102, A
21	42	41.6	661	US-09-252-991A-21459	Sequence 21459, A
22	41.5	41.1	236	US-09-634-955B-16	Sequence 16, Appl
23	41.5	41.1	294	US-09-252-991A-32328	Sequence 32328, A
24	41	40.6	149	US-09-732-210-306	Sequence 306, App
25	41	40.6	150	US-09-732-210-308	Sequence 308, App
26	41	40.6	151	US-09-732-210-183	Sequence 183, App
27	41	40.6	151	US-09-732-210-1385	Sequence 1385, Ap

28	41	40.6	151	US-09-732-210-1389	Sequence 1389, Ap
29	41	40.6	151	US-09-732-210-1402	Sequence 1402, Ap
30	41	40.6	256	US-09-252-991A-29587	Sequence 29587, A
31	41	40.6	313	US-09-252-991A-24305	Sequence 24305, A
32	41	40.6	349	US-09-252-991A-25831	Sequence 25831, A
33	41	40.6	388	US-09-252-991A-22751	Sequence 22751, A
34	41	40.6	464	US-09-252-991A-26212	Sequence 26212, A
35	41	40.6	510	US-09-252-991A-33084	Sequence 33084, A
36	41	40.6	749	US-09-562-737-98	Sequence 98, Appl
37	41	40.6	1018	US-08-072-610-2	Sequence 2, Appl
38	41	40.6	1018	US-08-719-822B-2	Sequence 2, Appl
39	41	40.6	1018	US-09-092-458-2	Sequence 2, Appl
40	41	40.6	1841	US-08-804-227C-6	Sequence 6, Appl
41	41	40.6	5215	US-09-105-537-2	Sequence 2, Appl
42	40.5	40.1	59	US-08-787-739-50	Sequence 50, Appl
43	40.5	40.1	59	US-09-178-115-50	Sequence 50, Appl
44	40.5	40.1	59	US-09-177-776-50	Sequence 50, Appl
45	40.5	40.1	98	US-08-481-658B-50	Sequence 50, Appl

ALIGNMENTS

```
RESULT 1
US-09-134-001C-5584
; Sequence 5584, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5584
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5584

Query Match      47.0%; Score 47.5; DB 4; Length 801;
Best Local Similarity 64.7%; Pred. No. 22;
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      1 EVEDPKVPEPAREGER 17
DB      244 EAEVPIVIEP-SRIEG 259

RESULT 2
US-09-163-748C-7
; Sequence 7, Application US/09163748C
; Patent No. 6509172
; GENERAL INFORMATION:
; APPLICANT: DeBaker, Oliver
; APPLICANT: Van den Bynde, Benoit
; APPLICANT: Boon-Fallour, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode Member Of The Gage
; FILE REFERENCE: LUD 5558
; CURRENT APPLICATION NUMBER: US/09/163,748C
; CURRENT FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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US-09-163-748C-7

Query Match 46.5%; Score 47; DB 4; Length 117;
Best Local Similarity 46.7%; Pred. No. 2.8;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDVVKVEPASEREG 17
Db 30 DEVEMIEPATREG 44

RESULT 3

US-09-252-991A-26148
; Sequence 26148, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26148
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26148

Query Match 46.0%; Score 46.5; DB 4; Length 571;
Best Local Similarity 64.7%; Pred. No. 21;
Matches 11; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 5 VP-KVEPASEREG 20
Db 74 VPVQVEPAAARQGER 90

RESULT 4

US-09-252-991A-32898
; Sequence 32898, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32898
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32898

Query Match 43.6%; Score 44; DB 4; Length 228;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 VEDVVKVEPASEREG 17
Db 74 VEHVGVVEPLSRGHG 89

RESULT 5

US-09-035-648-18
; Sequence 18, Application US/09035648
; Patent No. 6100031
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
; TITLE OF INVENTION: GROWTH AND PROLIFERATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,648
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/818,829
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/003001
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-035-648-18

Query Match 43.6%; Score 44; DB 3; Length 747;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 VEDVVKVEPASEREG 19
Db 51 VGDVFPQKPASTDREGDQ 68

RESULT 6

US-09-001-951-18
; Sequence 18, Application US/09001951
; Patent No. 6268470
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
; TITLE OF INVENTION: GROWTH AND PROLIFERATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US

ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/001,951
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/818,829
 FILING DATE: 14-MAR-1997
 APPLICATION NUMBER: 60/013,438
 FILING DATE: 15-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Melkielejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/003001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 747 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-09-001-951-18

Query Match 43.6%; Score 44; DB 3; Length 747;
 Best Local Similarity 50.0%; Pred. No. 72;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 2 VEDVPKVEPASPAREGGE 19
 DB 51 VGDVPFOLKPASDTEGDQ 68

RESULT 7
 US-08-818-829-18
 Sequence 18, Application US/08818829
 Patent No. 6458939
 GENERAL INFORMATION:
 APPLICANT: Shyjan, Andrew W.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 TITLE OF INVENTION: DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
 NUMBER OF INVENTION: GROWTH AND PROLIFERATION
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,829
 FILING DATE: 14-MAR-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/013,438
 FILING DATE: 15-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Melkielejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/003001
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 747 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-818-829-18

Query Match 43.6%; Score 44; DB 4; Length 747;
 Best Local Similarity 50.0%; Pred. No. 72;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 2 VEDVPKVEPASPAREGGE 19
 DB 51 VGDVPFOLKPASDTEGDQ 68

RESULT 8
 US-08-363-208-2
 Sequence 2, Application US/08363208
 Patent No. 5767366
 GENERAL INFORMATION:
 APPLICANT: Sathasivan, Kanagasabapathi
 TITLE OF INVENTION: A Mutant Acetolactate Synthase Gene From
 TITLE OF INVENTION: Arabidopsis Thaliana For Confering Imdazolnolone
 NUMBER OF INVENTION: Resistance To Crop Plants
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Llewellyn A. Proctor, Sr.
 STREET: 11481 Sheraton Drive
 CITY: Baton Rouge,
 STATE: LA
 COUNTRY: USA
 ZIP: 70815
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/363,208
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/657,429
 FILING DATE: 19-FEB-1991
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Proctor Sr., Llewellyn A.
 REGISTRATION NUMBER: 20,152
 REFERENCE/DOCKET NUMBER: 013911-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (504)275-8689
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 670 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-363-208-2

Query Match 42.6%; Score 43; DB 1; Length 670;
 Best Local Similarity 50.0%; Pred. No. 91;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EVEDVPKVEPAPA 12
 DB 227 DVEDIPRIIEEA 238

RESULT 9
US-09-137-478-2
Sequence 2, Application US/09137478
Patent No. 6225105
GENERAL INFORMATION:
APPLICANT: Sathasivan, Kanagasabapathi
APPLICANT: Murali, No. 6225105imoto
TITLE OF INVENTION: A Mutant Acetolactate Synthase Gene From
TITLE OF INVENTION: Arabidopsis thaliana For Conferring Imidazolinone
TITLE OF INVENTION: Resistance To Crop Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Llewellyn A. Proctor, Sr.
STREET: 11481 Sheraton Drive
CITY: Baton Rouge,
STATE: LA
COUNTRY: USA
ZIP: 70815
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,429
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Proctor Sr., Llewellyn A.
REGISTRATION NUMBER: 20,152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (504)275-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-137-478-2

Query Match 42.6%; Score 43; DB 3; Length 670;
Best Local Similarity 50.0%; Pred. No. 91;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEA 12
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Db 227 DVEDIPRIIEEA 238

RESULT 10
US-08-426-125-8
Sequence 8, Application US/08426125
Patent No. 5853973
GENERAL INFORMATION:
APPLICANT: Kakefuda, Genichi
APPLICANT: Otc, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu
APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide
TITLE OF INVENTION: Resistant Products
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,125
FILING DATE: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/0A674
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-527-7783
TELEFAX: (212)-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
US-08-426-125-8

Query Match 42.6%; Score 43; DB 2; Length 671;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEA 12
:||||:|
Db 227 DVEDIPRIIEEA 238

RESULT 11
US-08-455-355-8
Sequence 8, Application US/08455355
Patent No. 5928937
GENERAL INFORMATION:
APPLICANT: Kakefuda, Genichi
APPLICANT: Otc, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu
APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide
TITLE OF INVENTION: Resistant Products
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,355
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A674-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-527-7783

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; TELEFAX: (212)-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; US-08-455-355-8

Query Match          42.6%; Score 43; DB 2; Length 671;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 EYEDVPKVVPEA 12
DB      227 DVEDIPRIIEA 238

RESULT 12
US-09-367-512-7
; Sequence 7, Application US/09367512
; Patent No.: 6576455
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; APPLICANT: Kakefuda, Genichi
; APPLICANT: Otc, Karl-Heinz
; APPLICANT: Kwagh, Jae-Gyu
; APPLICANT: Stockton, Gerald W.
; TITLE OF INVENTION: Structure-Based Designed Herbicide Resistant
; FILE REFERENCE: 3489/1A674-US3
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 08/426,125
; PRIOR FILING DATE: 1995-04-20
; PRIOR APPLICATION NUMBER: 08/455,355
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: PCT/US96/05782
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-367-512-7

Query Match          42.6%; Score 43; DB 4; Length 671;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 EYEDVPKVVPEA 12
DB      227 DVEDIPRIIEA 238

RESULT 13
US-09-046-894-35
; Sequence 35, Application US/09046894
; Patent No.: 6190857
; GENERAL INFORMATION:
; APPLICANT: Ralph, David
; APPLICANT: An, Gang
; APPLICANT: O'Hara, Mark S.
; APPLICANT: Veltri, Robert
; TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA
; TITLE OF INVENTION: PROFILES IN PERIPHERAL LEUKOCYTES
; NUMBER OF SEQUENCES: 55

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,894
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,576
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakashima, Richard A.
; REGISTRATION NUMBER: P-42,023
; REFERENCE/DOCKET NUMBER: UROC:014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 761 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-046-894-35

Query Match          42.6%; Score 43; DB 3; Length 761;
Best Local Similarity 41.2%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      4 DVPKVVPEASEREGGER 20
DB      727 DTPATDPLSEKGGKK 743

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RESULT 14
US-08-933-750C-45
; Sequence 45, Application US/08933750C
; Patent No.: 5932442
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750C
; FILING DATE: September 23, 1997

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/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 811 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: L1VR1UT04
/ CLONE: 2515476
/
/ US-08-933-750C-45
/
Query Match 42.6%; Score 43; DB 2; Length 811;
Best Local Similarity 41.2%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 DVPKVEPASEREGGER 20
DB 777 DTPATSDPLSEKGGKK 793

RESULT 15
/ US-09-234-613-45
/ Sequence 45, Application US/09234613
/ Patent No. 6132973
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Shah, Puryi
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Yue, Henry
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
/ NUMBER OF SEQUENCES: 98
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/234,613
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/933,750
/ FILING DATE: September 23, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
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/ TELEX:
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 811 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: L1VR1UT04
/ CLONE: 2515476
/
/ US-09-234-613-45
/
Query Match 42.6%; Score 43; DB 3; Length 811;
Best Local Similarity 41.2%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 DVPKVEPASEREGGER 20
DB 777 DTPATSDPLSEKGGKK 793
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Search completed: August 1, 2003, 18:38:35
JOB time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2003, 18:22:55 ; Search time 41 Seconds
(without alignments)
77,428 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101

Sequence: 1 EVEDVPKYVERPASERGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	101	100.0	232	AA848317	T. pallidum ssp. p
3	101	100.0	312	AA848318	T. pallidum ssp. en
4	101	100.0	432	AA848316	T. pallidum ssp. p
5	97	96.0	20	AA848329	T. pallidum acidic
6	96	95.0	20	AA848328	T. pallidum acidic
7	87	86.1	20	AA848320	T. pallidum acidic
8	82	81.2	20	AA848330	T. pallidum acidic
9	77	76.2	20	AA848321	T. pallidum acidic

10	65	64.4	21	22	AA848325	T. pallidum acidic
11	60	59.4	19	22	AA848319	T. pallidum acidic
12	53	52.5	16	22	AA848326	T. pallidum acidic
13	50	49.5	79	21	AA661691	Arabidopsis thalia
14	50	49.5	187	21	AA616629	Arabidopsis thalia
15	50	49.5	187	21	AA650350	Arabidopsis thalia
16	49	48.5	266	22	AA839738	Human polyprotein
17	49	48.5	266	22	AA880279	Human prostate can
18	49	48.5	266	22	AA864379	Human prostate can
19	49	48.5	277	22	AA880305	Human prostate can
20	49	48.5	277	22	AA880347	Human prostate can
21	49	48.5	288	22	AA880343	Human prostate can
22	49	48.5	289	22	AA841524	Human polyprotein
23	49	48.5	304	21	AA857037	Human prostate can
24	48	47.5	296	22	ABG15624	Novel human diagno
25	47.5	47.0	792	22	AA882199	S. epidemidis ope
26	47.5	47.0	801	23	ABP40739	Scaphylococcus epi
27	47	46.5	1022	22	ABG02687	Novel human diagno
28	47	46.5	1278	24	ABG74682	Human CGPD protein
29	46	45.5	60	23	ABP34774	Human ORP3747 prot
30	46	45.5	171	21	AA808178	Arabidopsis thalia
31	46	45.5	197	21	AA808177	Arabidopsis thalia
32	46	45.5	226	21	AA808176	Arabidopsis thalia
33	45	44.6	197	21	AA859487	Arabidopsis thalia
34	45	44.6	226	21	AA859486	Arabidopsis thalia
35	45	44.6	286	21	AA859485	Arabidopsis thalia
36	44	43.6	57	22	AAU47716	Protonibacterium
37	44	43.6	71	22	ABG50059	Human liver peptid
38	44	43.6	71	22	AB830014	Peptide #2665 enco
39	44	43.6	71	22	AB835183	Peptide #2689 enco
40	44	43.6	71	22	AB820622	Protein #2621 enco
41	44	43.6	71	22	AA856018	Human brain expres
42	44	43.6	71	22	AA868385	Human bone marrow
43	44	43.6	71	22	AA816202	Peptide #2636 enco
44	44	43.6	71	22	AA828693	Peptide #2730 enco
45	44	43.6	71	22	AA803935	Peptide #2617 enco

ALIGNMENTS

RESULT 1
AA848327
ID AA848327 standard; peptide; 20 AA.
AC AA848327;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 9.
XX
KM Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KM yaws; bejel.
XX
OS Treponema pallidum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16425.
XX
PR 14-JUN-1999; 99US-0138981.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI, 2001-080711/09.
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological

PT sample -
XX
PS Claim 15; Fig 11; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein.
XX
SQ Sequence 20 AA;
XX
Query Match 100.0%; Score 101; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 3, 1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EVEDVPKVVPEASEREGER 20
DB 1 EVEDVPKVVPEASEREGER 20
XX
RESULT 2
AAB48317
ID AAB48317 standard; Protein; 232 AA.
XX
AC AAB48317;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum ssp. pertenue (CDC-2) acidic repeat protein (arp).
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX
OS Treponema pallidum ssp. pertenue.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
XX 14-JUN-2000; 2000MO-US16425.
XX
PF 14-JUN-1999; 99US-0138981.
XX
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PA Liu H, Steiner B, Rhodes B;
XX
PI WPI; 2001-080711/09.
XX
DR N-PSDB; AAC84648.
XX
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
XX Claim 15; Fig 8; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against

CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC The present sequence represents a T. pallidum subspecies pertenue
CC (CDC-2) arp protein.
XX
SQ Sequence 232 AA;
XX
Query Match 100.0%; Score 101; DB 22; Length 232;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EVEDVPKVVPEASEREGER 20
DB 128 EVEDVPKVVPEASEREGER 147
XX
RESULT 3
AAB48318
ID AAB48318 standard; Protein; 312 AA.
XX
AC AAB48318;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum ssp. endemicum (Bosnia) acidic repeat protein (arp).
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX
OS Treponema pallidum ssp. endemicum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
XX 14-JUN-2000; 2000MO-US16425.
XX
PF 14-JUN-1999; 99US-0138981.
XX
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PA Liu H, Steiner B, Rhodes B;
XX
PI WPI; 2001-080711/09.
XX
DR N-PSDB; AAC84649.
XX
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
XX Claim 15; Fig 10; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC The present sequence represents a T. pallidum subspecies endemicum
CC (Bosnia) arp protein.
XX
SQ Sequence 312 AA;
XX
Query Match 100.0%; Score 101; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EVEDVPKVVPEASEREGER 20

DB 128 EVEDVPKVVPEASEREGGER 147

RESULT 4

AAB48316 AAB48316 standard; Protein; 432 AA.

AC AAB48316;

DT 20-APR-2001 (first entry)

DE T. pallidum ssp. pallidum (Ni) acididic repeat protein (arp).

KM Treponema pallidum; acididic repeat protein; arp; immunogenic; syphilis;

OS Treponema pallidum ssp. pallidum.

PN WO200077486-A2.

PD 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US16425.

PR 14-JUN-1999; 99US-0138981.

PS (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Liu H, Steiner B, Rhodes B;

DR WPI; 2001-080711/09.

DR N-PSDB; AAC84647.

PT Detecting Treponema pallidum in blood, saliva, etc., by detecting

PS Claim 15; Fig 6; 73pp; English.

CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-Treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acididic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC The present sequence represents a T. pallidum subspecies pallidum
CC (Ni) arp protein.

SQ Sequence 432 AA;

Query Match 100.0%; Score 101; DB 22; Length 432;

Best Local Similarity 100.0%; Pred. No. 1e-07; 0; Indels 0; Gaps 0;

DT 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 EVEDVPKVVPEASEREGGER 20

168 EVEDVPKVVPEASEREGGER 187

RESULT 5

AAB48329

DT 20-APR-2001 (first entry)

DE T. pallidum acididic repeat protein immunogenic peptide arp 11.

KM Treponema pallidum; acididic repeat protein; arp; immunogenic; syphilis;

OS Treponema pallidum.

PN WO200077486-A2.

PD 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US16425.

PR 14-JUN-1999; 99US-0138981.

PS (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Liu H, Steiner B, Rhodes B;

DR WPI; 2001-080711/09.

PT Detecting Treponema pallidum in blood, saliva, etc., by detecting

PS Claim 15; Fig 11; 73pp; English.

CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-Treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acididic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein.

SQ Sequence 20 AA;

Query Match 96.0%; Score 97; DB 22; Length 20;

Best Local Similarity 95.0%; Pred. No. 1.4e-08; 1; Indels 0; Gaps 0;

DT 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 EVEDVPKVVPEASEREGGER 20

1 EVEDVPKVVPEASEREGGER 20

RESULT 6

AAB48328

DT 20-APR-2001 (first entry)

DE T. pallidum acididic repeat protein immunogenic peptide arp 10.

KM Treponema pallidum; acididic repeat protein; arp; immunogenic; syphilis;

OS Treponema pallidum.

PN WO200077486-A2.

PD 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US16425.

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RR      14-JUN-1999;      99US-0138981.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
PI      Liu H, Steiner B, Rhodes B;
XX
XX      WPI; 2001-080711/09.
XX
XX      Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT      formation of a complex between immunogenic peptides of acidic repeat
PT      protein of the bacterium and an antibody present in the biological
PT      sample -
XX
XX      Claim 15; Fig 11; 73pp; English.
PS
XX
XX      The invention relates to a method of detecting presence of Treponema
CC      pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC      sample that involves contacting an acidic repeat protein (arp), or one
CC      or more isolated immunogenic TP peptides of arp with an Ab containing
CC      biological sample and then detecting the formation of a complex between
CC      immunogenic peptides and Ab. The presence of the complex indicates the
CC      presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC      and bejel diseases. The immunogenic peptides or the Abs raised against
CC      arp, as part of an immunogenic composition, are useful for inducing a
CC      protective immune response against syphilis, yaws or bejel caused by TP.
CC      Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC      arp protein.
XX
XX      Sequence      20 AA;
SQ
XX
XX      Query Match      95.0%;      Score 96;      DB 22;      Length 20;
XX      Best Local Similarity      95.0%;      Pred. No. 2e-08;
XX      Matches      19;      Conservative      1;      Mismatches      0;      Indels      0;      Gaps      0;
XX
XX      1      EVEDYKRYVEPASEREGGER      20
QY      |||:|||||||
DB      1      EVENVKRYVEPASEREGGER      20
XX
XX      RESULT 7
XX      ID      AAB48320      standard; peptide; 20 AA.
XX
XX      AAB48320;
XX
XX      20-APR-2001      (first entry)
XX
XX      T. pallidum acidic repeat protein immunogenic peptide arp 2.
DE
XX
XX      Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
XX      yaws; bejel.
XX
XX      Treponema pallidum.
XX
XX      WO200077486-A2.
XX
XX      21-DEC-2000.
XX
XX      14-JUN-2000; 2000MO-US16425.
XX
XX      14-JUN-1999; 99US-0138981.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX      Liu H, Steiner B, Rhodes B;
PI
XX
XX      WPI; 2001-080711/09.
XX
XX      Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT      formation of a complex between immunogenic peptides of acidic repeat
PT      protein of the bacterium and an antibody present in the biological
PT      sample -
XX

```

PS Claim 15; Fig 11; 73pp; English.

CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein.

CC

XX Sequence 20 AA;

SQ

Query Match 86.1%; Score 87; DB 22; Length 20;
Best Local Similarity 94.4%; Pred. No. 5,4e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EVEDVPKVVPEPASEEGG 18
||| ||| ||| ||| |||
Db 3 EVEDAPKVVEPAASREGG 20

RESULT 8
AAB48330
ID AAB48330 standard; peptide; 20 AA.
AC AAB48330;
XX
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 12.
KW Treponema pallidum, acidic repeat protein; arp; immunogenic; syphilis;
XX yaws; bejel.
XX
OS Treponema pallidum.
PN WO200077486-A2.
XX
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16425.
XX
PR 14-JUN-1999; 99US-0138981.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
PI Liu H, Steiner B, Rhodes B;
XX
XX WPI; 2001-080711/09.
DR

XX Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
XX
XX Claim 15; Fig 11; 73pp; English.

The invention relates to a method of detecting presence of Treponema
pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
sample that involves contacting an acidic repeat protein (arp), or one
or more isolated immunogenic TP peptides of arp with an Ab containing
biological sample and then detecting the formation of a complex between
immunogenic peptides and Ab. The presence of the complex indicates the
presence of TP. The method is thus useful for diagnosing syphilis, yaws,
and bejel diseases. The immunogenic peptides or the Abs raised against
arp, as part of an immunogenic composition, are useful for inducing a
protective immune response against syphilis, yaws or bejel caused by TP.
Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
arp protein.


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OS Treponema pallidum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16425.
XX
PR 14-JUN-1999; 99US-0138981.
XX
PS (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR MPI; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
PS Claim 15; Fig 11; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein.
XX
SQ Sequence 19 AA;
XX
Query Match 59.4%; Score 60; DB 22; Length 19;
Best Local Similarity 92.3%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 EVEDVVKVVEPAS 13
DB 7 EVEDAPKVVVEPAS 19
XX
RESULT 12
AAB48326
ID AAB48326 standard; peptide; 26 AA.
XX
AC AAB48326;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 8.
XX
KM Treponema pallidum, acidic repeat protein; arp; immunogenic; syphilis;
KM yaws; bejel.
XX
OS Treponema pallidum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16425.
XX
PR 14-JUN-1999; 99US-0138981.
XX
PS (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;

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XX
DR MPI; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
PS Claim 15; Fig 11; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein.
XX
SQ Sequence 26 AA;
XX
Query Match 52.5%; Score 53; DB 22; Length 26;
Best Local Similarity 84.6%; Pred. No. 0.21;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 8 VVEPASEREGER 20
DB 1 VVEPASGHEGGER 13
XX
RESULT 13
AAG61691
ID AAG61691 standard; Protein; 79 AA.
XX
AC AAG61691;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80063.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-01231825.
XX
PR 05-MAR-1999; 99US-0123180.
XX
PR 09-MAR-1999; 99US-0123548.
XX
PR 23-MAR-1999; 99US-0125788.
XX
PR 25-MAR-1999; 99US-0126264.
XX
PR 29-MAR-1999; 99US-0126785.
XX
PR 01-APR-1999; 99US-0127462.
XX
PR 06-APR-1999; 99US-0128234.
XX
PR 08-APR-1999; 99US-0128714.
XX
PR 16-APR-1999; 99US-0129845.
XX
PR 19-APR-1999; 99US-0130077.
XX
PR 21-APR-1999; 99US-0130449.
XX
PR 23-APR-1999; 99US-0130510.
XX
PR 23-APR-1999; 99US-0130891.
XX
PR 28-APR-1999; 99US-0131449.
XX
PR 30-APR-1999; 99US-0132048.
XX
PR 30-APR-1999; 99US-0132407.

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PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	07-MAY-1999;	99US-0132487.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142801.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	21-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
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PR	27-AUG-1999;	99US-0151065.
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PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
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Query Match 49.5%; Score 50; DB 21; Length 79;
Best Local Similarity 62.5%; Pred. No. 2.2;
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Db 21 IPVPEPPELERSGER 36

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AC
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 17348.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301339.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 49.5%; Score 50; DB 21; Length 187;
 Best Local Similarity 62.5%; Pred. No. 5.8;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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 Db 21 IPVPEPELEERSGER 36

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 DT 18-OCT-2000 (first entry)
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 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63797.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
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Query Match	49.5%	Score 50	DB 21	Length 187
Best Local Similarity	62.5%	Pred. No. 5.8		
Matches 10	Conservative 1	Mismatches 5	Indels 0	Gaps 0

```
Qy      5 VPKVVEPASEREGGER. 20
         : | | | | | | |
Db      21 IPVPEPELERESGGER 36
```

Search completed: August 1, 2003, 18:27:25
Job time : 43 secs

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